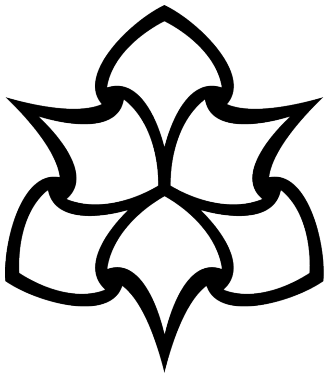

16S rRNA gene pyrosequencing indicate that siblings of Crohn's disease patients exhibit a biologically relevant dysbiosis in the mucosal microbiota communities

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Background: Reduced mucosal concentrations of *Faecalibacterium prausnitzii* predict disease recurrence in patients with Crohn's disease (CD). Siblings of CD patients have elevated risk of developing disease and share aspects of disease phenotype compared with healthy controls (HC), including a dysbiosis in the faecal microbiota [1]. No study has compared the mucosal microbiota in CD siblings to unrelated healthy controls.

Aim: To apply 16S rRNA gene pyrosequencing in order to determine whether dysbiosis is present in the mucosal microbiota of siblings of CD patients with reference to HC, and to accomplish a more comprehensive characterisation of that dysbiosis.

Methods: Rectal biopsies were taken from 21 patients with quiescent CD, 17 of their healthy siblings and 19 unrelated healthy controls (HC). Total DNA was extracted using a phenol/ chloroform based method. PCR amplification of the V1 to V3 region of the bacterial 16S ribosomal RNA gene was performed, and microbiota composition resolved by 454 pyrosequencing.

Results: For each group, resulting species in the microbiota were classified into those that were common and abundant among similar subjects (core) versus infrequent and rare. [2] In terms of both microbial diversity (measured by both the Shannon Wiener and Simpson's indexes of diversity) and species richness, the core mucosal microbiota of both siblings and CD patients were significantly less diverse than HC. Although the diversity of the rare microbiota was lower in CD compared with HC, there were no differences in diversity of rare microbiota between siblings and HC. Metacommunity profiling using the Bray Curtis (SBC) index of similarity with unweighted pair group averages showed that the core microbial metacommunity of siblings was more similar to CD patients (SBC=0.70) than to HC, whereas the rare microbial metacommunity of siblings was more similar to HC (SBC=0.42). As in patients with CD, the species that contributed most to the dissimilarity between healthy siblings and HC was *F. prausnitzii*, Table 1.

Conclusions: This is the first in depth case control study of the mucosal microbiota in the siblings of CD patients. We report a dysbiosis that is characterised by reduced diversity of core microbiota and lower abundance of *F. prausnitzii*. Given that siblings of CD patients have elevated risk of developing CD, this dysbiosis in otherwise healthy people implicates microbiological processes in CD pathogenesis and risk.